



RESULT 15  
 AF042091/c  
 LOCUS AF042091  
 DEFINITION Homo sapiens chromosome 21q22.3 PAC 267010, complete sequence.  
 ACCESSION AF042091  
 NID 92829109  
 KEYWORDS Htg.  
 SOURCE Human.  
 ORGANISM Homo sapiens  
 Eukaryota: Metazoa: Chordata: Vertebrata: Mammalia: Eutheria:  
 Primates: Catarrhini: Hominoidea: Homo.  
 /RPT\_FAMILY "AluY45"  
 /EVIDENCE NOT\_EXPERIMENTAL  
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 /EVIDENCE NOT\_EXPERIMENTAL  
 exon 152953..153051  
 /NOTE "M2EF, score = 67.3%"  
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 repeat\_region 152953..153254  
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 repeat\_region 153261..153298  
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 /EVIDENCE NOT\_EXPERIMENTAL  
 exon complement(153269..153313)  
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 complement(153386..153751)  
 /RPT\_FAMILY "THE1B"  
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 exon 153485..153555  
 /NOTE "GRAIL, score = 62.000%", comment = good"  
 /EVIDENCE NOT\_EXPERIMENTAL  
 exon 153870..153969  
 /NOTE "M2EF, score = 46.9%"  
 /EVIDENCE NOT\_EXPERIMENTAL  
 exon 153870..153969  
 /NOTE "GRAIL, score = 99.000%", comment = excellent"  
 /EVIDENCE NOT\_EXPERIMENTAL  
 repeat\_region 156920..155396  
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 /NOTE "M2EF, score = 52.2%"  
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 exon 48810 a 30519 c 30142 g 45936 t  
 ORIGIN  
 BASE COUNT  
 Query Match 4.7%; Score 307.2; DB 42; Length 155407;  
 Best Local Similarity 89.7%; Pred. No. 2.3e-48; Length 155407;  
 Matches 330; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
 QY 1654 tccttgaatgtggactccaaaattatttctgtgtttatgtaaagttggtaatcg 1713  
 DB 2884 TTCTCTCAGATGGAACTCCAAATTATTTCTGCTTGTAGAAAGTGGTGAATCG 2825  
 QY 1714 cagagccgttccctttagtgcacgtggaaacatcttggccacatcaatgtgg 1773  
 DB 2824 CAGGCCGTTCCCTATATGCCAGTAAAGGAAACCTTGGCCACGATCACGTTGA 2765  
 exon 4528..4541  
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 exon 4528..4541  
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 repeat\_region 1714..1773  
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 repeat\_region complement(5542..5923)  
 /RPT\_FAMILY "L1PA12"  
 /EVIDENCE NOT\_EXPERIMENTAL  
 repeat\_region complement(6481..8905)  
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 exon complement(6995..7113)  
 /NOTE "GRAIL, score = 62.000%", comment = good"  
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 exon complement(7525..7650)  
 /NOTE "GRAIL, score = 76.000%", comment = excellent"  
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 repeat\_region complement(8892..9257)  
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 /EVIDENCE NOT\_EXPERIMENTAL  
 exon complement(9253..9383)  
 /NOTE "GRAIL, score = 66.000%", comment = good"  
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 repeat\_region complement(9256..9595)  
 /RPT\_FAMILY "L1"  
 /EVIDENCE NOT\_EXPERIMENTAL  
 repeat\_region complement(9505..9685)  
 /RPT\_FAMILY "L1M4"  
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  /rpt_family="THE1B"
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  complement(84212, .85874)
  /rpt_family="L1PA2"
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  88416, .88764
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repeat_region 96662. .97124
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  complement(96735. .96868)
  /rpt_family="L1M3"
  /evidence="not_experimental"
repeat_region 98030. .98995
  /rpt_family="L1PA10"
  /evidence="not_experimental"
  complement(98239. .98562)
  /evidence="not_experimental"
repeat_region 98693. .98823
  exon
    /note="GRAIL, score = 89.000%, comment = excellent"
    complement(99131. .99682)
    /rpt_family="L1HE1B"
    /evidence="not_experimental"
    complement(99161. .99033)
    /note="MZF, score = 46.4%"
    /evidence="not_experimental"
    complement(100874. .100555)
    /note="GRAIL, score = 61.000%, comment = good"
    /evidence="not_experimental"
    complement(101701. .102079)
    /evidence="not_experimental"
    complement(101949. .101033)
    /note="GRAIL, score = 71.000%, comment = good shadow"
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    complement(101957. .102172)
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    complement(106111. .108110)
    /rpt_family="L1M8"
    /evidence="not_experimental"
    complement(108145. .108421)
repeat_region 105198. .105306
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    /evidence="not_experimental"
    complement(117935. .118085)
    /note="GRAIL, score = 99.000%, comment = excellent shadow"
repeat_region 117936. .118085
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repeat_region 118285. .118383
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    /note="Xpound exon prediction, score = 87.000%, comment = excellent"
    /evidence="not_experimental"
    complement(118249. .118332)
    /note="GRAIL, score = 87.000%, comment = excellent"
repeat_region 118350. .118383
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Page 67

Search completed: July 23, 1999, 12:05:32  
Job time: 4690 sec